SEQUENCE LISTING

<110> Issa, Jean-Pierre

<120> CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND METHODS OF USE THEREFOR

<130> JHU1590

<140> 09/398,522
<141> 1999-09-15

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ggaagcccca ggggcgcagg ggaagcgggg ctcgcgccgg gcggggtttc cctgcgcccc    180
ggcgcccccc gggcagcatg cccctgcggg caggggggag c tgggctgaac tggccctccc  240
gggggctcag cttgcgccct agagcccacc agatgtgccc ccgccggggc ccccgggttg    300
cgtgaggaca cctcctctga ggggcgccgc ttgcccctct ccggatcgcc cggggccccg    360
gctggccaga gg atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg     411
             Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser
              1               5                  10
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gga cag ccc cgg agc ttc atg cgg ctc aac gac ctg tcg ggg gcc ggg      459
Gly Gln Pro Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly
     15                  20                  25

ggc cgg ccg ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac      507
Gly Arg Pro Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp
 30                  35                  40                  45

tcc gag gcg gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc      555
Ser Glu Ala Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe
                 50                  55                  60

ttc tac ttg agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg      603
Phe Tyr Leu Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr
             65                  70                  75

gtc tgt aac ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc      651
Val Cys Asn Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu
         80                  85                  90

aac tgc gtg acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt      699
Asn Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys
     95                  100                 105

gac tcc cag cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt      747
Asp Ser Gln Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe
110                 115                 120                 125

gcc ttc ttt gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc      795
Ala Phe Phe Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile
                130                 135                 140

ttt ggg aaa aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt      843
Phe Gly Lys Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe
            145                 150                 155

ttc atc gtc atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac      891
Phe Ile Val Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn
        160                 165                 170

gtc agc ttc tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg      939
Val Ser Phe Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg
    175                 180                 185

gcc att aac cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg      987
Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu
190                 195                 200                 205

gat acg ctg ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc     1035
Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val
                210                 215                 220

ttc ttc atc ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt     1083
Phe Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu
            225                 230                 235

cgg aac cga tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg     1131
Arg Asn Arg Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val
        240                 245                 250
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gac ctg gag cgc tat tac cag aca gag aac gag gat gag agc ccc ttc      1179
Asp Leu Glu Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe
    255                 260                 265

atc tgc tcc cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg      1227
Ile Cys Ser Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val
270                 275                 280                 285

ccc acg ctg cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac      1275
Pro Thr Leu Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp
                290                 295                 300

tat gag gcc tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac      1323
Tyr Glu Ala Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn
            305                 310                 315

cag tac tac acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc      1371
Gln Tyr Tyr Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly
        320                 325                 330

gcc atc aac ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag      1419
Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln
    335                 340                 345

gtc atc acg ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat      1467
Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp
350                 355                 360                 365

gct cat tcc ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg      1515
Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val
                370                 375                 380

ggc tcc ttc ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag      1563
Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln
            385                 390                 395

ttc tca gag acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt      1611
Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg
        400                 405                 410

gtg cgg ttc ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc      1659
Val Arg Phe Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro
    415                 420                 425

ggc agc tgc tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt      1707
Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg
430                 435                 440                 445

aag gca gcc cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg      1755
Lys Ala Ala Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg
                450                 455                 460

gtt ggg ctg ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag      1803
Val Gly Leu Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln
            465                 470                 475

ccc agc agc agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac      1851
Pro Ser Ser Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His
        480                 485                 490
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ctg gtg cac cac cac cac cac cat cac cac cac tac cac ctg ggc aat     1899
Leu Val His His His His His His His His His Tyr His Leu Gly Asn
    495                 500                 505

ggg acg ctc agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat     1947
Gly Thr Leu Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp
510                 515                 520                 525

gcc aat ggg tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc     1995
Ala Asn Gly Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala
                530                 535                 540

ctc tcc ggg gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac     2043
Leu Ser Gly Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr
            545                 550                 555

cat gcc gac tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc     2091
His Ala Asp Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro
        560                 565                 570

agg tcc cca tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg     2139
Arg Ser Pro Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val
    575                 580                 585

tat ccc acc gtg cac acc agc cct cca ccg gag acg ctg aag gag aag     2187
Tyr Pro Thr Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys
590                 595                 600                 605

gca cta gta gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc     2235
Ala Leu Val Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser
                610                 615                 620

ctc aac atc cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag     2283
Leu Asn Ile Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu
            625                 630                 635

aca cag agt aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct     2331
Thr Gln Ser Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro
        640                 645                 650

tgc ttg aaa gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac     2379
Cys Leu Lys Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr
    655                 660                 665

tgt gcc cgg gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg     2427
Cys Ala Arg Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met
670                 675                 680                 685

cct gac tca gac agc gag gca gtt tat gag ttc aca cag gat gcc cag     2475
Pro Asp Ser Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln
                690                 695                 700

cac agc gac ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc     2523
His Ser Asp Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly
            705                 710                 715

cca gat gca gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt     2571
Pro Asp Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys
        720                 725                 730
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gac acc ttc cga aag att gtg gac agc aag tac ttt ggc cgg gga atc      2619
Asp Thr Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile
    735                 740                 745

atg atc gcc atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac      2667
Met Ile Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His
750                 755                 760                 765

gag cag ccc gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc      2715
Glu Gln Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val
                770                 775                 780

ttc acc agc ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat      2763
Phe Thr Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr
            785                 790                 795

ggt ccc ttt ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc      2811
Gly Pro Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val
        800                 805                 810

att gtg gtc atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc      2859
Ile Val Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly
    815                 820                 825

ctg tcg gtg ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg      2907
Leu Ser Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val
830                 835                 840                 845

cgc ttc ctg ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc      2955
Arg Phe Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr
                850                 855                 860

atg gac aac gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc      3003
Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe
            865                 870                 875

atc ttc agc atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct      3051
Ile Phe Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser
        880                 885                 890

gag cgg gat ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg      3099
Glu Arg Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu
    895                 900                 905

ctc tgg gcc atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg      3147
Leu Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp
910                 915                 920                 925

aac aaa gtc ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc      3195
Asn Lys Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala
                930                 935                 940

ctt tat ttc att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat      3243
Leu Tyr Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn
            945                 950                 955

ttg ctg gtc gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc      3291
Leu Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala
        960                 965                 970
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aac aag tcc gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt      3339
Asn Lys Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly
    975                 980                 985

gat ggg gac agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac      3387
Asp Gly Asp Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His
990                 995                 1000                1005

ccg gag ctg cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc      3435
Pro Glu Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala
                1010                1015                1020

gcc aca ccc atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag      3483
Ala Thr Pro Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu
            1025                1030                1035

gcg ctg ggc cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag      3531
Ala Leu Gly Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu
        1040                1045                1050

cct ggg gcg gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct      3579
Pro Gly Ala Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser
    1055                1060                1065

ccg cac agc ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc      3627
Pro His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser
1070                1075                1080                1085

agc cgg aac agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca      3675
Ser Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro
                1090                1095                1100

agt gga gag cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag      3723
Ser Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln
            1105                1110                1115

gat gaa gag gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt      3771
Asp Glu Glu Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser
        1120                1125                1130

gac cat cgc cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt      3819
Asp His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe
    1135                1140                1145

gac ctg cca gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt      3867
Asp Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser
1150                1155                1160                1165

ggc cga ggg tct gct tct gag cac cag gac tgc aat ggc aag tcg gct      3915
Gly Arg Gly Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala
                1170                1175                1180

tca ggg cgc ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat      3963
Ser Gly Arg Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp
            1185                1190                1195

ggg gat gac gcc gat gac gag ggc aac ctg                              3993
Gly Asp Asp Ala Asp Asp Glu Gly Asn Leu
        1200                1205
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<210> 52
<211> 1207
<212> PRT
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<220>
<223> CACNA1G - a gene ecoding a T-type calcium channel

<400> 52

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Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
            20                  25                  30
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
        35                  40                  45
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
    50                  55                  60
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65                  70                  75                  80
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                85                  90                  95
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
    290                 295                 300
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400
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Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
405 410 415
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
420 425 430
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
435 440 445
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
450 455 460
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465 470 475 480
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
485 490 495
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
500 505 510
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
515 520 525
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
530 535 540
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545 550 555 560
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
565 570 575
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
580 585 590
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
595 600 605
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610 615 620
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625 630 635 640
Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
645 650 655
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
660 665 670
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
675 680 685
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
690 695 700
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
705 710 715 720
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
725 730 735
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
740 745 750
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
755 760 765
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
770 775 780
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785 790 795 800
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
805 810 815
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
820 825 830
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
835 840 845
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
850 855 860
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865 870 875 880

Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
885 890 895
Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
900 905 910
Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
915 920 925
Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
930 935 940
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945 950 955 960
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
965 970 975
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
980 985 990
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
995 1000 1005
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
1010 1015 1020
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025 1030 1035 1040
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
1045 1050 1055
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
1060 1065 1070
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
1075 1080 1085
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
1090 1095 1100
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
1105 1110 1115 1120
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
1125 1130 1135
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
1140 1145 1150
Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
1155 1160 1165
Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
1170 1175 1180
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
1185 1190 1195 1200
Ala Asp Asp Glu Gly Asn Leu
1205

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<220>
<223> primer for PCR (GAPDH)

<400> 53
cggagtcaac ggattggtcg tat 23

<210> 54
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> primer for PCR (GAPDH)

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agccttctcc atggtggtga agac 24

<210> 55
<211> 22
<212> DNA
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<220>
<223> Target sequence for bisulfite-PCR primer

<400> 55
aaaaaaccca aactacaaaa ac 22

<210> 56
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<223> r = G or A

<400> 56
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<220>
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<400> 57
aactatcycc aacyccacaa 20

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<221> misc_feature
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aagagatttt ttttttttt tttrgt 26

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<220>
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<221> misc_feature
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<223> y = C or T

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aaaatccyaa aaaaaacycc ccc 23

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<220>
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<223> r = G or A

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<400> 61
aacyatccct ccctctaacc tac 23

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<220>
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<400> 62
aggtagtatg gtgaggtttg tttt 24

<210> 63
<211> 22
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<223> r = G or A

<400> 63
atcaatacta aacraaatca aa 22

<210> 64
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<400> 64
aggaaaagaa aggtaaggg 19

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caaaattaac rcaataaaaa aa 22

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tatttgaaga ggtggggaaa 20

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aaactcttac cccacctaac c 21

<210> 68
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<210> 69
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<400> 69
ccactaactc aaaactaaaa aa 22

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gggaggtgta aaaggatgaa a 21

<210> 71
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<220>
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<400> 71
ctaacactaa aataaaaata aa 22

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gtaggatgtt ataygaagag 20

<210> 73
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<220>
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<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 73
aaacrctaac raacatacta c 21

<210> 74
<211> 20
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<220>
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<400> 74
gggttttttt tagggtattt 20

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<223> r = G or A

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gaattaaatt tcaaaaaaac cr 22

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<210> 77

<211> 22
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<221> misc_feature
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<223> r = G or A

<400> 77
aaaaaaccta acraaacact ta 22

<210> 78
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<400> 78
gttattgtgt agtggagttt gg 22

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<223> r = G or A

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<223> y = C or T

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<400> 81
tccctaaatt ccacacatt 19

<210> 82
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<213> Artificial Sequence

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<400> 82
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<210> 83
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<221> misc_feature
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<223> r = G or A

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gttttggttt tggttgtg 18

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<400> 85
ccactaccaa acaaatcccc 20

<210> 86
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<400> 86
tttattgggg aatttcggg 19

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<400> 92
gttttttaa gattgggttt ttttag 26

<210> 93
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caaaccccaa acatccttta tcca 24

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ggatttaggg gtaaggggag gg 22

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<223> r = G or A

<400> 95
aaaaaccaca actaaaatcc ratt 24

<210> 96
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<220>
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<400> 96
agtgagggat ttagttgtgg tgtg 24

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
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<223> r = G or A

<400> 97
aactatcrcc aacrccacaa 20

<210> 98
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<220>
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<221> misc_feature
<222> (0)...(0)
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<400> 98
aagagatttt tttttttttt tttygt 26

<210> 99
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<210> 100
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<223> y = C or T

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<210> 101
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<400> 101
aacaaaatac aactcccaaa caccc 25

<210> 102
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<220>
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<400> 102
ttagggtttg atttttaaat ttggtt 26

<210> 103
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<223> r = G or A

<400> 103
caaaaaatta cratcccccc tc 22

<210> 104
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<220>
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<221> misc_feature
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<223> y = C or T

<400> 104
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<210> 105
<211> 576
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
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<400> 105
ccccgggaggc gcccttggga ccttttgcaa tcctggcgct cttgcagcct gggcttccta 60
taaatggggt gcgggcgccg gccgcgcatt cgcaccgggа cctgcggggc tgagtgcccc 120
tctcggttgc tgccgctgag gagcccgccc agccagccag ggccgcgagg ccgaggccag 180
gccgcagccc aggagccgcc ccaccgcagc tggcgatgga cccgccgagg cccgcgctgc 240
tggcgctgcc tgcgctgctg ctgctgctgc tggcggggcgc cagggccggt gagtgcgcgg 300
ccgctctgcg ggcagcagag ggagcgggag ggagccggcg gaccgaggtt ggccgggggca 360
gcctgggcct aggccagagg gagggcagcc acagggtcca gggcgagtgg ggggattgga 420
ccagctggcg gcccctgcag gctcaggatg ggggggcgcgg gatggagggg ctgaggaggg 480
ggtctccgga gcctgcctcc ctcctgaaag gtgaaacctg tgccggtggt ccccctgtcg 540
ggcccctagc acccgctggg aagacgtggg aagctc 576

<210> 106
<211> 2093
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> CACNA1G CpG ISLAND

<400> 106
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ttggctccag ccttcgggag cggacccagg ggcaaggggа ggggagaggg gcggtcctgg 180
gttttggggt gggaatcgga ttccagctgt ggttctctcc ctgcgctccc gcccgcactg 240
ccacggcgga cggccaatgg gcgcgcggct cggggccggc ggcgtccggc gattggctgc 300
ggggctgtct gggggcgggg ccgaggcttg aagttgaagt gagggatcca gctgtggtgt 360
gcgcgggggt cctcgccgcc gctttcgctc gctcgctccg cgtctcggcc ggaggaggag 420
gctgtggcgc cggcgacagc tacggcagcg gcagccaccg cggcggctgc ggcggcggca 480
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tgagcccgcg gcggggcggg ggaaggagcc gcccccaccc cctccaagcc cacccctaaa 600
gagatcccтc ctcccctccc ccgccgcctg gcgcggagcc gggacgatgc tgacccctta 660
gatccggctc cagctgcgcc gcgggaagag ggggcgcccc tccccggacc cccgcctccc 720
gccgctgccc ccctttcgt tcgccctctc ggggcggctt cgccgaaggt agcgccgaat 780
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gccgggggtca gcagaaaagg acccgggcag cgcggactcc gaggcggagg ggctgccgta 1260
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cctcgcgggt tggaggcaca acaaggagat tccggcggcg gctgatgtca ggggcgcaga 1980
atgagaacaa gatgtggtgg aggggagctg tctgcccccg gagctgggag tggagcccct 2040
ttccgctaga gcccagtgcc gcgggtgcct cctacccgat ctccattcga tgc 2093

<210> 107
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> CDX2 CpG Island

<400> 107
ctcgttaatc acggaagccg ccggcctggg gctccgcacg ccagcctgtg cgggtcttcc 60
ccgcctctgc agcctagtgg gaaggaggtg ggaggaaaga aggaagaaag ggagggaggg 120
aggaggcagg ccagagggag ggaccgcctc ggaggcagaa gagccgcgag gagccagcgg 180
agcaccgcgg gctgggggcgc agccaccgc cgctcctcga gtcccctcgc cccttтccct 240
tcgtgccccc cggcagcctc cagcgtcggt ccccaggcag catggtgagg tctgctcccg 300
gtccctcgcc accatgtacg tgagcta 327

<210> 108
<211> 1663
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> EGFR CpG Island

<400> 108
gtccgcgggg accgggtcca gaggggcagt gctgggaacg ccccтctcgg aaattaactc 60
ctcagggcac cgctcccctc ccatgcgccg ccccactccc gccggagact aggtcccgcg 120
ggggccaccg tgtccaccgc ctcgcggccg ctggccttgg gtccccgctg ctggttctcc 180
tccctcctcc tcgcattcta ctcctcctct gctcctcccg atcccctcta cgccgcctgg 240
tccctcctcc tccgcccctg cctccgcgc ctcggcccgc gcgagctaga cgtccgggca 300
gccccgggcg cagcgcggcc gcagcagcct cctcccccg cacggtgtga gcgcccgccg 360
cgccgaggcg gccggagtcc cgagctagcc ccgcggccgc cgccgcccag accggacgac 420
aggccacctc gtcgcgtccg cccgagtccc cgcctcgccg ccaacgccac aaccaccgcg 480
cacggccccc tgactccgtc cagtattgat cgggagagcc ggagcgagct cttcggggag 540
cagcgatgcg accctccggg acggccgggg cagcgctcct ggcgctgctg gctgcgctct 600
gcccggcgag tcgggctctg gaggaaaaga aaggtaaggg cgtgtctcgc ggctcccgc 660
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cccgcgcccc cgcccgtcct ttcctgtttc cttgagatca cgtgcgccgc cgaccgggac 780
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cccgaaccgc tcccaacttt cttccctcac tttccccgcc cagctgcgca ggatcggcgt 960
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gcgctgtctt cccagggcgc gacggggtcc tggcgcgcac ccgagggccg ctgcccaccc 1080
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caggtggggt ccgacccgcc ccttgggcgc agaccccggc cgctcgcctc gccccgtgcg 1440
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cgcgccgaaa gccccaggct ctccttcgat ggccgcctcg cggagacgtc cgggtctgct 1560
ccacctgcag cccttcggtc gcgcctgggc ttcgcggtgg agcgggacgc ggctgtccgg 1620
ccactgcagg gggggatcgc gggactcttg agcggaagcc ccg 1663

<210> 109
<211> 1787
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> FBN1 CpG Island

<221> misc_feature
<222> (1)...(1787)
<223> n = A,T,C or G

<400> 109
agagccgcgt ctggagtggg ctctcgacac ccagggcaag tgggggcggc agagccctct 60
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tcccggcctc cggcgtctgc tgagtgtccg gcgggagagg cgcagggagc gcgctaccgg 180
gaggcgcggg cagcggggac tggttttctc tcgggccagg gcctccgggg caaccgtctc 240
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cgggagaggt taatctcgga tctaaacctc gcagccgcag agcgggctaa aaccgctact 360
ccacctcttc ccatttctcc cctccccacc tcaagacaaa aagtcccagg ccgggcagga 420
cctgatcacc tctgcctcct cccactgcgc taatcctgcg agcgagaggc cccgcaccga 480
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gatgagggcg acgaaggagg gggtgtcatt ttcttttttt ttcttttttt aaaaaaagta 600
tttctctcgc gagaaaccgc tgcgcggacg atacttgaag aggtggggaa aggagggggc 660
tgcgggagcc gcggcagaga ctgtgggtgc cacaagcgga caggagccac agctgggaca 720
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ccgcgctctt ctggcggggc ccgggaggcg agggattggc cggggctgct gcgccggggc 1260
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caggcggccg acnggttggg ctttgggaat ggggaccgcg agcttcagca tcccgatgcc 1380
ctgaaagtct cccgcctcg gggatttgtc tctgtgttgc agctggcagg ggccgcctga 1440
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gggcgcggca agaggcggcg ggagccggtg gcggctcggc atcatgcgtc gagggcgtct 1620
gctggagatc gccctgggat ttaccgtgct tttagcgtcc tacacgagcc atggggcgga 1680
cgccaatttg gaggctggga acgtgaagga aaccagagcc agtcgggcca agagaagagg 1740
cggtggagga cacgacgcgc ttaaagggta aaggaaccgg ttccctc 1787

<210> 110
<211> 810
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> GPR37 CpG Island

<400> 110
tccegccccg caccegcccc tagcccgggc tcggggacct gtcaggctgg tttcgacagc 60
tggggaatta acctgtcccg cccatcccta gcctcgagcc gcgcaggctc cgcgcctccg 120
cccttgttcc ctcccagctc ctccgagtgg aagccgctac aaatggcttg aatgaaacgt 180
gtgtgggttt agtgagtggt gaaccaccag gggatcccgt ctccccacaa accagtatct 240
ctccgaggag gaggcgaagg agtgggagga ggcaacgagc cgagagtcga gcttcgcggg 300
cgcgcgcagc ggctggagcg cgggggcgag gccgggccac ctccccttcc cggccgcgca 360
ctgcctggcc cgcggcggtt ccaggcacca cccttcccgt ccgggctgag cccgctgtgg 420
cagtgactag ctcccgcggc tagcggcact gtccaccgac gagcggcgcc ctcttctccc 480
ccttctcccc acgatttcct tctctgcggc ggcacgccgt ccagcagcct gcttcgcccc 540
gtcgtcaact ttgagctgga ggagaagcaa ctttggcagt ggccgcgggg ttggaatccc 600
gcttctcctc ggcagcagta ggctcgcaag tcgctggggt taggtggggc aagagtttcg 660
ccggcgcatc agcgctgctt cggactgttt gcaacgtgtt tccagcgagc tgggagcggg 720
gttgtgactg cgagtcgtct gggggagggg gacttgtttt tcttttcctc tagagacctc 780
ggcttgcaac tggatcaaac gctgtcgaaa 810

<210> 111
<211> 550
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> HSPA6 CpG Island

<400> 111
tgtattcgca tggtaacata tcttcggtct tcctgccgct gggctctcag cggcctccca 60
aggcagcccg caggcccgtg ctcgcctcag ggatcctcca cagccccggg gagaccttgc 120
ctctaaagtt gctgcttttg cagctctgcc acaaccgcgc gtcctcagag ccagccggga 180
ggagctagaa ccttcccccc gtttctttca gcagccctga gtcagaggcg ggctggcctt 240
gcaagtagcc gcccagcctt cttcggtctc acggaccgat ccgccccgaac cttctccccg 300
ggtcagcgcc gcgctgcgcc gcccggctga ctcagcccgg gcgggcgggc gggaggctct 360
cgactgggcg ggaaggtgcg ggaaggttcg cggcggcggg gtcggggagg tgcaaaagga 420
tgaaaagccc gtggacggag ctgagcagat ccggccgggc tggcggcaga gaaaccgcag 480
ggagagcctc actgctgagc gcccctcgac gcgggcggca gcagcctccg tggcctccag 540
catccgacaa 550

<210> 112
<211> 278
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> IQGAP2 CpG Island

<400> 112
agagttcact tttacttcag tgtcagcgcg cggcggccgt ggctggctct ggcgagagag 60

caccgaggga gtgggtcgca gatcttcggg cggctagggg aaatcggcga gaggcgggat 120
ccgagcgcgc cggcgggggcg cagagcccgc gagcctggcc agcgagggta gccgcggggg 180
gcgcgccccg ggcgggcccc cggagacgcg caggatgcca cacgaagagc tgccgtcgct 240
gcagagaccc cgctatggct ctattgtgga cgatgaaa 278

<210> 113
<211> 1461
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> KL CpG Island

<400> 113
ctcgaaagag gggcgcgggt gggcgcgtct ccccgcgagc atctcaccta aggggaatc 60
cctttcagcg cacggcgaag ttccccctcg gctgtcccac ctggcagtcc ctctaggatt 120
tcggccagtc cctaattggc tccagcaatg tccagccgga gcttctttgg gcctccgagt 180
gggagaaaag tgagagcagg tgcttcccca gcggcgcgct ccgctagggc ccggcaggat 240
cccgcccccа agtcgggaaa agttggtcgg cgccttttct ccccgacgaa gccgctccag 300
ggctgctctc agaggacgcg cggcaggcaa agagaatgaa cctgagcgtc cacgaaacgt 360
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tgcccccacc cccagtgcca gggcggaggc agtcccggct cgcaggtaat tattgccagc 540
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gcgggcataa aggggcgcgg cgcgggggccc cggagcctgg ctcccgcgca gcatgcccgc 660
cagcgccccg ccgcgccgcc cgccggccgcc gccgccgtcg ctgtcgctgc tgctggtgct 720
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cttccgccac ttcggcggtc aggtcaagta ctggatcacc atcgacaacc cctacgtggt 1380
ggcctggcac ggctacgcca ccgggcgcct ggccccggc atccggggca gcccgcggct 1440
cgggtacctg gtggcgcaca a 1461

<210> 114
<211> 249
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> PAR2 CpG Island

<400> 114
cccggggcgt ggcctcccgc aggtgagtac gctgctcctt cggtttccct gaaacctaac 60
ccgccctggg gaggcgcgca gcagaggctc cgattcgggg caggtgagag gctgacttcc 120
tctcggtgcg tccagtggag ctctgagttt cgaatcggcg gcggcggatt ccccgcgcgc 180
ccggcgtcgg ggcttccagg aggatgcgga gccccagcgc ggcgtggctg ctgggggccg 240
ccatcctgc 249

<210> 115

<211> 709
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> PITX2 CpG Island

<400> 115
agtccgtgct cctgctcctc ggttggctcc taagtgcccc gccaggtccc ctctcctttc 60
gctctcccgg ctccggctcc cgactcttcg gcccgctggc atctgcttcc ctcccctgcc 120
tcgtttctcg tcgcccctgc tcgctccccc cggcgctcgc ccgggcgctg tgctcgctcc 180
tggatcgcca gccgcgcagc cgggctcggc cggccgcccg cgcgccactg tgcagtggag 240
tttggtggaa tctctgctga cgtcacgtca ctccccacac ggagtaggag cagagggaag 300
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gcttgccgtg cagccggagg ctcggctcgc tggaaatcgc cccgggaagc agtgggacgc 540
ggagacagca gctctctccc ggtagccgat aacggggaaa tggagaccaa ctgccgcaaa 600
ctggtgtcgg cgtgtctgca attagagaaa gataaaagcc agcaggggaa gaatgaggac 660
gtgggcgccg aggacccgtc taagaagaag cggcaaaggc ggcagcgga 709

<210> 116
<211> 1496
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> PTCA CpG Island

<221> misc_feature
<222> (1)...(1496)
<223> n = A,T,C or G

<400> 116
gcggccgcag cggcagcagc gcccgccgtg tgagcagcag cagcggctgg tctgtcaacc 60
ggagcccgag cccgagcagc ctgcggccag cagcgtcctc gcaagccgag cgcccaggcg 120
cgccaggagc ccgcagcagc ggcagcagcg cgccgggccg cccgggaagc ctccgtcccc 180
gcggcggcgg cggcggcggc ggcaacatgg cctcggctgg taacgccgcc gagccccagg 240
accgcggcgg cggcggcagc ggctgtatcg gtgccccggg acggccggct ggaggcggga 300
ggcgcagacg gacgggggcg ctgcgccgtg ctgccgcgcc ggaccgggac tatctgcacc 360
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gactntntcn ttcccacttt ntcttcccnt acctntaact cntnggggat cgccccgcc 480
acacacaaac acacacactn tcttcctctn tntctcacac acaacacaca cactcactca 540
cacntctnca ggaaaagcag cagacaaatg gggattgaaa aattcaaacc ctcctctgg 600
tnntgggagg aaagggctgt ctgaggtccg caggggtgg aggtgtgtgt gtgtgcgtgt 660
gtgtgtgtgn anacacacgc cctccctggt gtgccttttc cggagcactg gaaagccgtc 720
cacggcggac cacctcaagg gcggccgcgc ggtcgtagcg gtagtagcgt tcgtcgtgtg 780
agtagtagta gcggttggtt tgttaatcgg agttcgagtt cgagtagttt gcggttagta 840
gcgttttcgt aagtcgagcg tttaggcgcg ttaggagttc gtagtagcgg tagtagcgcg 900
tcgggtcgtt cgggaagttt tcgttttcgc ggcggcggcg gcggcggcgg taatatggtt 960
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gagnagattt nttanggnng gtattttaga ttntnttntt tttatttttnt ttttttntat 1200
ttntaatttn tnggggatcg ttttcgttat atataaatat atatattntt ttttttttn 1260
ttttatatat aatatatata tttatttata tntttntagg aaaagtagta gataaatggg 1320

gattgaaaaa tttaaatttt ttttttggtn ntgggaggaa agggttgttt gaggttcgta 1380
gggggtggag gtgtgtgtgt gtgcgtgtgt gtgtgtgnan atatacgttt tttttggtgt 1440
gttttttcg gagtattgga aagtcgttta cggcggatta ttttaagggc ggtcgt 1496

<210> 117
<211> 701
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> PTCHB CpG Island

<221> misc_feature
<222> (1)...(701)
<223> n = A,T,C or G

<400> 117
gcggccgcgg cactgtcctg ccccgtgccc cctgccctga acttcttcct cctgcgcccc 60
tgccccctatt tgcagcctaa actcctgtac ggctgccaca tttcttaaca tcttggaggg 120
ggaggcggag tggagagagg cggagagagg aaggggggag ggagccgaaa taaaggtggt 180
ttcctttttt ggcagccagt tttggttttg ttgagcatga aatctctgct cccttaaaaa 240
attattctcg gaaaaagata tccccccegt tttccaggtt ttgagccgcc tctccttagg 300
gcctggtcgg gggaggaaaa gttgtaaaca aattgccacc ttaaattcgc ggtgcgantc 360
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aggcgagcac ccagacgggg gcccgccggg gcgcggccca gcgccgggga aatgccgcgc 480
cggggagcag catgcgccgg cctgagccct tcccttttgca ctcggctgtt ttttacgttt 540
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tattgtcgta agttgcagct ggctgcccca nttcctaatt cagctcacac agcntntccc 660
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<210> 118
<211> 273
<212> DNA
<213> Homo sapiens

<220>
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<222> (0)...(0)
<223> SDC1 CpG Island

<400> 118
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gagcatcgag cagcggaacc cgcgaagccg gcccgcagcc gcgacccgcg cagcctgccg 180
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<210> 119
<211> 751
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> SDC4 CpG Island

<400> 119

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<210> 120
<211> 673
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment termed MINT31

<221> misc_feature
<222> (1)...(673)
<223> n = A,T,C or G

<400> 120
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gcacggggtt caagactcag gcgccgcata ctcagaatga gagcagagac tcccgccagg 180
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ctccgctccc ggg 673